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(54) **Detection of maize fungal pathogens using the polymerase chain reaction**

(57) Internal Transcribed Spacer (ITS) DNA sequences from the ribosomal RNA gene region are described for different species and strains of *Helminthosporium carbonum*, *Helminthosporium turcicum*,

Helminthosporium maydis, *Cercospora zea-maydis*, *Kabatiella zea* and *Puccinia sorghi*. Specific primers from within these sequences are identified as being useful for the identification of the fungal isolates using PCR-based techniques.

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Description

The present invention relates to the use of species-specific primers in polymerase chain reaction assays for the detection of fungal pathogens of maize. The use of these primers enables the detection of specific isolates of fungal pathogens and the monitoring of disease development in plant populations.

Diseases in plants cause considerable crop loss from year to year resulting both in economic deprivation to farmers and, in many parts of the world, to shortfalls in the nutritional provision for local populations. The widespread use of fungicides has provided considerable security against plant pathogen attack. However, despite \$1 billion worth of expenditure on fungicides, worldwide crop losses amounted to approximately 10% of crop value in 1981 (James, 1981; *Seed Sci. & Technol.* 9: 679-685).

The severity of the destructive process of disease depends on the aggressiveness of the pathogen and the response of the host. One aim of most plant breeding programs is to increase the resistance of host plants to disease. Typically, different races of pathogens interact with different varieties of the same crop species differentially, and many sources of host resistance only protect against specific pathogen races. Furthermore, some pathogen races show early signs of disease symptoms, but cause little damage to the crop. Jones and Clifford (1983; *Cereal Diseases*, John Wiley) report that virulent forms of the pathogen are expected to emerge in the pathogen population in response to the introduction of resistance into host cultivars and that it is therefore necessary to monitor pathogen populations. In addition, there are several documented cases of the evolution of fungal strains that are resistant to particular fungicides. As early as 1981, Fletcher and Wolfe (1981; *Proc. 1981 Brit. Crop Prot. Conf.*) contended that 24% of the powdery mildew populations from spring barley and 53% from winter barley showed considerable variation in response to the fungicide triadimenol and that the distribution of these populations varied between varieties, with the most susceptible variety also giving the highest incidence of less susceptible types. Similar variation in the sensitivity of fungi to fungicides has been documented for wheat mildew (also to triadimenol), *Botrytis* (to benomyl), *Pyrenophora* (to organomercury), *Pseudocercospora* (to MBC-type fungicides) and *Mycosphaerella fijiensis* to triazoles to mention just a few (Jones and Clifford; *Cereal Diseases*, John Wiley, 1983).

The three most important cereal crops in the world are maize (corn), rice and wheat (1973; *Compendium of Corn Diseases*, Amer. Phytopath. Soc. page 1). There are a great number of fungi, bacteria, and viruses that are pathogenic to maize, causing 9.4 % annual worldwide losses. In the corn belt of the United States, maize reduction because of disease infection is between 7 to 17% annually. Maize is the most important native American plant, and the U.S. produces about 44% of the world's 250 million metric tons annual production.

The major infectious diseases of maize are caused by fungi and include rusts, smuts, downy mildews, rots, spots, blights and deformations (1973; *Compendium of Corn Diseases*, Amer. Phytopath. Soc. page 13). Although fungal diseases are usually diagnosed by the structures produced by the pathogens, the differential symptomology caused by different isolates and species of these fungi make the accurate predictive determination of potential disease loss difficult. Consequently, the availability of improved diagnostic techniques for the rapid and accurate identification of specific pathogens will be of considerable use to field pathologists.

There are three primary species of *Helminthosporium* pathogenic to maize causing foliar diseases. *Helminthosporium carbonum* causes helminthosporium leaf spot (blight), also known as northern leaf spot (1973; *Compendium of Corn Diseases*, Amer. Phytopath. Soc. page 17). It is distributed throughout the Americas, southeast Asia, southeast Europe, south and central Africa, and India (Jones and Clifford; *Cereal Diseases*, John Wiley, 1983). There are two primary physiologically-based races. Race 1 is highly virulent on maize, causing a charred appearance on the ear's kernels. Race 2 tends to be less virulent than race 1 and does not display host specificity. Race 2 produces a host-specific toxin. *Helminthosporium maydis* causes southern leaf blight in maize. It occurs worldwide in warm (20-32°C), humid climates. In the United States, it is found in the southeastern and midwestern states (Jones and Clifford; *Cereal Diseases*, John Wiley, 1983). The disease was originally thought to be of little economic importance until a severe 1970 epidemic in the U.S. resulted in large losses. Northern leaf blight (turicum leaf blight) is caused by *Helminthosporium turicum*. The disease develops in humid areas of the world where maize is grown (1973; *Compendium of Corn Diseases*, Amer. Phytopath. Soc. page 16). Moderate temperatures (18-27°C) and heavy dews during the growing season promote severe disease development in which 50% losses of grain can occur. Typical control of these diseases include the use of fungicides, crop rotation, burning crop debris, and breeding resistant hybrids and varieties.

Kabatiella zeae is another significant maize foliar pathogen causing eyespot disease. The disease originally reported as brown eyespot in Japan has also been found in Canada, Argentina, Austria, France, Germany, Yugoslavia, New Zealand and in several north-central U.S. states and Pennsylvania (1973; *Compendium of Corn Diseases*, Amer. Phytopath. Soc. page 21). The disease may develop on sheaths and outer husks, but lesions are more concentrated on leaves approaching maturity. In extremely infected plants, kernel infections may also develop. Cool, humid weather favors disease development. Disease control measures include the use of less susceptible hybrids, fungicides, and clean plowing or crop rotation.

Cercospora or gray leaf spot is caused by *Cercospora zeae-maydis* and infects maize, barnyardgrass, Johnson-

grass and other *Sorghum* species (1973; Compendium of Corn Diseases, Amer. Phytopath. Soc. page 24). The disease is prevalent in warm-to-hot, humid areas of the United States, Mexico, Central America, northern South America, Europe, Africa, southeast Asia, India, China, and the Philippines. The disease has increased in severity in recent years in the southeastern and mid-Atlantic states of the U.S. especially in areas using minimum tillage of maize and no crop rotation (Latterell and Rossi, 1983; *Plant Disease*. Vol. 67, No. 8: 842-847). The disease can spread from the leaf sheaths to the stalk in highly infected plants. This can cause stalk deterioration to the point where lodging precludes mechanical harvesting. Crop rotation, resistant cultivars and fungicides are currently used to control gray leaf spot.

Puccinia sorghi causes common maize rust and can be found wherever maize is grown. Infection can occur on any plant parts above ground but is mainly found on the leaves (1973; Compendium of Corn Diseases, Amer. Phytopath. Soc. page 24). Cooler temperatures (16-23°C) and high moisture contribute to the proliferation of the disease. Under severe infection conditions, chlorosis and death of the leaves and sheaths may occur ultimately reducing cereal yield.

Thus, there is a real need for the development of technology that will allow the identification of specific races of pathogen fungi early in the infection process. By identifying the specific race of a pathogen before disease symptoms become evident in the crop stand, the agriculturist can assess the likely effects of further development of the pathogen in the crop variety in which it has been identified and can choose an appropriate fungicide if such application is deemed necessary.

Additionally, with the increasing need for DNA fingerprinting, restriction fragment length polymorphism (RFLP) analysis, Southern transfers and PCR analysis, the isolation of high molecular weight DNA becomes a major problem when attempting to process a large number of plant samples in a timely manner. Several methods for the isolation of DNA have been reported, all of which have drawbacks for various reasons. These include DNA losses due to degradation and adsorption, the co-isolation of PCR inhibiting contaminants and labor extensive and costly protocols. Therefore, there is a need for a DNA extraction method which isolates high molecular weight DNA for high throughput analysis using molecular biology methods.

The present invention is drawn to methods of identification of different pathotypes of plant pathogenic fungi. The invention provides Internal Transcribed Spacer (ITS) DNA sequences that show variability between different fungal pathotypes. In a preferred embodiment, the invention provides ITS1 and ITS2 DNA sequences for the pathogens *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zea-maydis*, *Kabatella zae*, and *Puccinia sorghi*. Such DNA sequences are useful in the method of the invention as they can be used to derive primers for use in polymerase chain reaction (PCR)-based diagnostic assays. These primers generate unique fragments in PCR reactions in which the DNA template is provided by specific fungal pathotypes and can thus be used to identify the presence or absence of specific pathotypes in host plant material before the onset of disease symptoms.

This invention provides the possibility of assessing potential damage in a specific crop variety-pathogen strain relationship and of utilizing judiciously the diverse armory of fungicides which is available. Furthermore, the invention can be used to provide detailed information on the development and spread of specific pathogen races over extended geographical areas. The invention provides a method of detection that is especially suitable for diseases with a long latent phase. In addition, a method is described for extracting DNA from plant tissue for high throughput PCR analysis. Kits useful in the practice of the invention are also provided. The kits find particular use in the identification of the pathogens *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zea-maydis*, *Kabatella zae*, and *Puccinia sorghi*.

Figure 1 Sequence Alignment of the ITS regions from *Cercospora zea-maydis*, *Helminthosporium maydis*, *Helminthosporium carbonum*, and two isolates of *Helminthosporium turcicum*.

Figure 2 Sequence Alignment of the ITS regions from *Kabatella zae* isolates 18594 and 5125 and from clone pCRKZ56351(5-1).

Figure 3 Sequence Alignment of the ITS regions from clone pCRHMAY11534(4-1), from *Helminthosporium maydis* isolate 11534, from clone pCRHMAY24772(2-1), and from *Helminthosporium maydis* isolate 6921.

Figure 4 Sequence Alignment of the ITS regions from clone pCRHTUR26306(3-1) and from *Helminthosporium turcicum* isolates 26306, 6586, and 6402.

Figure 5 Sequence Alignment of the ITS regions from *Cercospora zea-maydis* isolate 5860 and from clones pCRCZMPOS12(2-1) and pCRCZLAD3-1(4-3).

Figure 6 Sequence Alignment of the ITS regions from clone pCRHCAR16185(5-2) and from *Helminthosporium carbonum* isolates 16185 and 5870.

SEQ ID NO:1 DNA sequence of the ITS region from *Cercospora zea-maydis* isolate #Ladder 3-1 (clone pCRCZLAD3-1(4-3)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.

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- SEQ ID NO:2 DNA sequence of the ITS region from *Cercospora zeae-maydis* isolate #POS 12 (clone pCRCZMPOS12(2-1)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- 5 SEQ ID NO:3 DNA sequence of the ITS region from *Kabatella zeae* isolate #56351 (clone pCRKZ56351(5-1)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- SEQ ID NO:4 DNA sequence of the ITS region from *Helminthosporium maydis* isolate #24772 (clone pCRHMAY24772(2-1)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- 10 SEQ ID NO:5 DNA sequence of the ITS region from *Helminthosporium maydis* isolate #11534 (clone pCRHMAY11534(4-1)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- 15 SEQ ID NO:6 DNA sequence of the ITS region from *Helminthosporium turcicum* isolate #26306 (clone pCRHTUR26306(3-1)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- 20 SEQ ID NO:7 DNA sequence of the ITS region from *Helminthosporium carbonum* isolate #16185 (clone CRHCAR16185(5-2)), comprising in the 5' to 3' direction: 3' end of small subunit rRNA gene, Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- 25 SEQ ID NO:8 DNA sequence of the ITS region from *Puccinia sorghi* (GenBank accession #L08734), comprising in the 5' to 3' direction: partial sequence of Internal Transcribed Spacer 1, 5.8S rRNA gene, Internal Transcribed Spacer 2, and 5' end of large subunit rRNA gene.
- SEQ ID NO:9 Oligonucleotide Primer ITS 1.
- SEQ ID NO:10 Oligonucleotide Primer ITS2.
- SEQ ID NO:11 Oligonucleotide Primer ITS3.
- 30 SEQ ID NO:12 Oligonucleotide Primer ITS4.
- SEQ ID NO:13 M13 Universal-20 Primer.
- SEQ ID NO:14 Reverse Primer used in Example 2.
- SEQ ID NO:15 Oligonucleotide Primer JB586.
- SEQ ID NO:16 Oligonucleotide Primer JB587.
- 35 SEQ ID NO:17 Oligonucleotide Primer JB588.
- SEQ ID NO:18 Oligonucleotide Primer JB589.
- SEQ ID NO:19 Oligonucleotide Primer JB590.
- SEQ ID NO:20 Oligonucleotide Primer JB591.
- SEQ ID NO:21 Oligonucleotide Primer JB592.
- 40 SEQ ID NO:22 Oligonucleotide Primer JB593.
- SEQ ID NO:23 Oligonucleotide Primer JB594.
- SEQ ID NO:24 Oligonucleotide Primer JB595.
- SEQ ID NO:25 Oligonucleotide Primer JB596.
- SEQ ID NO:26 Oligonucleotide Primer JB597.
- 45 SEQ ID NO:27 Oligonucleotide Primer JB598.
- SEQ ID NO:28 Oligonucleotide Primer JB615.
- SEQ ID NO:29 Oligonucleotide Primer JB616.
- SEQ ID NO:30 Oligonucleotide Primer JB617.
- SEQ ID NO:31 Oligonucleotide Primer JB618.
- 50 SEQ ID NO:32 Oligonucleotide Primer JB619.
- SEQ ID NO:33 Oligonucleotide Primer JB620.
- SEQ ID NO:34 Oligonucleotide Primer JB621.
- SEQ ID NO:35 Oligonucleotide Primer JB622.
- SEQ ID NO:36 Oligonucleotide Primer JB623.
- 55 SEQ ID NO:37 Oligonucleotide Primer JB624.
- SEQ ID NO:38 Oligonucleotide Primer JB625.
- SEQ ID NO:39 Oligonucleotide Primer JB626.
- SEQ ID NO:40 Oligonucleotide Primer JB627.

SEQ ID NO:41 Oligonucleotide Primer JB628.

The present invention provides unique DNA sequences that are useful in identifying different pathotypes of plant pathogenic fungi. Particularly, the DNA sequences can be used as primers in PCR-based analysis for the identification of fungal pathotypes. The DNA sequences of the invention include the Internal Transcribed Spacer (ITS) sequences of the ribosomal RNA gene regions of particular fungal pathogens as well as primers derived from these regions that are capable of identifying the particular pathogen. These ITS DNA sequences from different pathotypes within a pathogen species or genus, which vary between the different members of the species or genus, can be used to identify those specific members.

Biomedical researchers have used PCR-based techniques for some time and with moderate success to detect pathogens in infected animal tissues. Only recently, however, has this technique been applied to detect plant pathogens. The presence of *Gaumannomyces graminis* in infected wheat has been detected using PCR of sequences specific to the pathogen mitochondrial genome (Schlesser *et al.*, 1991; *Applied and Environ. Microbiol.* 57: 553-556), and random amplified polymorphic DNA (*i.e.* RAPD) markers were able to distinguish numerous races of *Gremmeniella abietina*, the causal agent of scleroderma canker in conifers. More recently, primers from within DNA sequences from the ITS of the ribosomal RNA gene region of strains of *Septoria*, *Pseudocercospora*, *Fusarium*, and *Mycosphaerella* have been identified as being useful for the identification of the fungal isolates using PCR-based techniques (WO 95/29260, herein incorporated by reference in its entirety.)

Ribosomal genes are suitable for use as molecular probe targets because of their high copy number. Despite the high conservation between mature rRNA sequences, the non-transcribed and transcribed spacer sequences are usually poorly conserved and are thus suitable as target sequences for the detection of recent evolutionary divergence. Fungal rRNA genes are organized in units, each of which encodes three mature subunits of 18S (small subunit), 5.8S, and 28S (large subunit). These subunits are separated by two Internal Transcribed Spacers, ITS1 and ITS2, of around 300 bp (White *et al.*, 1990; In: PCR Protocols; Eds.: Innes *et al.*; pages 315-322). In addition, the transcriptional units are separated by non-transcribed spacer sequences (NTSs). The ITS and NTS sequences are particularly suitable for the detection of specific pathotypes of different fungal pathogens.

The DNA sequences of the invention are from the Internal Transcribed Spacer sequences of the ribosomal RNA gene region of different plant pathogens. The ITS DNA sequences from different pathotypes within a pathogen species or genus vary among the different members of the species or genus. Once having determined the ITS sequences of a pathogen, these sequences can be aligned with other ITS sequences. In this manner, primers can be derived from the ITS sequences. That is, primers can be designed based on regions within the ITS sequences that contain the greatest differences in sequence among the fungal pathotypes. These sequences and primers based on these sequences can be used to identify specific pathogens and even specific pathotypes within a given pathogen species.

Particular DNA sequences of interest include ITS1 and ITS2 DNA sequences from *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zeae-maydis*, *Kabatella zeae* and *Puccinia sorghi*. Examples of such ITS DNA sequences are disclosed in SEQ ID Nos: 1 - 8. However, isolates of these organisms other than the isolates described herein may have minor sequence variations in their ITS regions. The present invention is intended to encompass the ITS DNA sequences of any isolates of these fungal pathogens. Sequences of oligonucleotide primers of interest are disclosed in SEQ ID Nos: 9-41. The sequences find use in the PCR-based identification of the pathotypes of interest.

Methods for the use of the primer sequences of the invention in PCR analysis are well known in the art. For example, see U.S. Patent Nos. 4,683,195 and 4,683,202, as well as Schlesser *et al.* (1991) *Applied and Environ. Microbiol.* 57: 553-556. See also, Nazar *et al.* (1991; *Physiol. and Molec. Plant Pathol.* 39: 1-11), which used PCR amplification to exploit differences in the ITS regions of *Verticillium albo-atrum* and *Verticillium dahliae* and therefore distinguish between the two species; and Johanson and Jeger (1993; *Mycol. Res.* 97: 670-674), who used similar techniques to distinguish the banana pathogens *Mycosphaerella fijiensis* and *Mycosphaerella musicola*.

The ITS DNA sequences of the invention can be cloned from fungal pathogens by methods known in the art. In general, the methods for the isolation of DNA from fungal isolates are known. See, Raeder & Broda (1985) *Letters in Applied Microbiology* 2:17-20; Lee *et al.* (1990) *Fungal Genetics Newsletter* 35:23-24; and Lee and Taylor (1990) In: *PCR Protocols: A Guide to Methods and Applications*, Innes *et al.* (Eds.); pages 282-287.

Alternatively, the ITS sequences of interest can be determined by PCR amplification. In an exemplified embodiment, primers to amplify the entire ITS sequence were designed according to White *et al.* (1990; In: PCR Protocols; Eds.: Innes *et al.* pages 315-322), and the amplified ITS sequence was subcloned into the pCR11 cloning vector. The subcloned sequence included the left hand ITS (ITS1), the right hand ITS (ITS2), as well as the centrally located 5.8S rRNA gene. This was undertaken for *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zeae-maydis*, and *Kabatella zeae*.

The ITS sequences were determined and the sequences were compared within each pathogen group to locate divergences that might be useful to test in PCR to distinguish the different species and/or strains. The ITS DNA se-

quences that were determined are shown in SEQ ID Nos: 1-7 as well as in Figures 1-6. From the identification of divergences, numerous primers were synthesized and tested in PCR-amplification. Templates used for PCR-amplification testing were firstly purified pathogen DNA, and subsequently DNA isolated from infected host plant tissue. Thus, it was possible to identify pairs of primers that were diagnostic, i.e. that identified one particular pathogen species or strain but not another species or strain of the same pathogen.

Preferred primer combinations are able to distinguish between the different species or strains in infected host tissue, i.e. host tissue that has previously been infected with a specific pathogen species or strain. This invention provides numerous primer combinations that fulfill this criterion for different *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zeae-maydis*, *Kabatiella zeae*, and *Puccinia sorghi*. The primers of the invention are designed based on sequence differences among the fungal ITS regions. A minimum of one base pair difference between sequences can permit design of a discriminatory primer. Primers designed to a specific fungal DNA's ITS region can be used in combination with a primer made to a conserved sequence region within the ribosomal DNA's coding region to amplify species-specific PCR fragments. In general, primers should have a theoretical melting temperature between about 60 to about 70 degree °C to achieve good sensitivity and should be void of significant secondary structure and 3' overlaps between primer combinations. Primers are generally at least about 5-10 nucleotide bases long.

The present invention lends itself readily to the preparation of "kits" containing the elements necessary to carry out the process. Such a kit may comprise a carrier being compartmentalized to receive in close confinement therein one or more containers, such as tubes or vials. One of the containers may contain unlabeled or detectably labeled DNA primers. The labeled DNA primers may be present in lyophilized form or in an appropriate buffer as necessary. One or more containers may contain one or more enzymes or reagents to be utilized in PCR reactions. These enzymes may be present by themselves or in mixtures, in lyophilized form or in appropriate buffers.

Finally, the kit may contain all of the additional elements necessary to carry out the technique of the invention, such as buffers, extraction reagents, enzymes, pipettes, plates, nucleic acids, nucleoside triphosphates, filter paper, gel materials, transfer materials, autoradiography supplies, and the like.

The examples below show typical experimental protocols that can be used in the isolation of ITS sequences, the selection of suitable primer sequences, the testing of primers for selective and diagnostic efficacy, and the use of such primers for disease and fungal isolate detection. Such examples are provided by way of illustration and not by way of limitation.

Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning: A Laboratory manual*, Cold Spring Harbor laboratory, Cold Spring Harbor, NY (1989) and by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al.*, *Current Protocols in Molecular Biology*, pub. by Greene Publishing Assoc. and Wiley-Interscience (1987).

Example 1: Fungal Isolates and Genomic Fungal DNA Extraction

See Table 1 for a listing of the fungal isolates used and their source. Fungi except for *Puccinia sorghi* were grown in 150 ml potato dextrose broth inoculated with mycelial fragments from PDA (Potato Dextrose Agar) cultures. Cultures were incubated on an orbital shaker at 28°C for 7-11 days. Mycelia were pelleted by centrifugation and then ground in liquid nitrogen and total genomic DNA extracted using the protocol of Lee and Taylor (1990; In: *PCR Protocols: A Guide to Methods and Applications*; Eds.: Innes *et al.*; pages 282-287). Since *P. sorghi* is an obligate biotroph and could therefore not be cultured on PDA, DNA was isolated from its spores from an infected maize leaf and ground with a Kontes pestle.

Table 1:

Source of Test Isolates			
Fungus	Isolate	Origin	Source
<i>Helminthosporium maydis</i> ¹	6921	Illinois	C. Naidoo ²
<i>Helminthosporium maydis</i>	XXXX	Illinois	C. Naidoo
<i>Helminthosporium maydis</i>	5654	Illinois	C. Naidoo

¹Syn. *Bipolaris maydis*, *Drechslera maydis*

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Table 1: (continued)

Source of Test Isolates			
Fungus	Isolate	Origin	Source
<i>Helminthosporium maydis</i>	11534	Maryland	ATCC ³
<i>Helminthosporium maydis</i>	4709	Indiana	C. Naidoo
<i>Helminthosporium maydis</i> , Race 1, mating type A	24772	North Carolina	ATCC ³
<i>Helminthosporium turcicum</i> ⁴	6810	Iowa	C. Naidoo
<i>Helminthosporium turcicum</i>	6830	Minnesota	C. Naidoo
<i>Helminthosporium turcicum</i> , Race 2	6402	Illinois	C. Naidoo
<i>Helminthosporium turcicum</i>	6870	Texas	C. Naidoo
<i>Helminthosporium turcicum</i> , Race 1	6586	Illinois	C. Naidoo
<i>Helminthosporium turcicum</i>	26306	Illinois	ATCC
<i>Helminthosporium turcicum</i> , Race 2	6294	Indiana	C. Naidoo
<i>Helminthosporium turcicum</i> , Race 2	5352	Ohio	C. Naidoo
<i>Helminthosporium carbonum</i> ⁵	5870	Illinois	C. Naidoo
<i>Helminthosporium carbonum</i>	6164	Iowa	C. Naidoo
<i>Helminthosporium carbonum</i>	6330	Nebraska	C. Naidoo
<i>Helminthosporium carbonum</i>	6378	Iowa	C. Naidoo
<i>Helminthosporium carbonum</i>	16185	Virginia	ATCC
<i>Kabatiella zaeae</i>	18594	Wisconsin	ATCC
<i>Kabatiella zaeae</i>	5125	Indiana	C. Naidoo
<i>Kabatiella zaeae</i>	56344	Wisconsin	ATCC
<i>Kabatiella zaeae</i>	56351	Michigan	ATCC
<i>Kabatiella zaeae</i>	6823	Minnesota	C. Naidoo
<i>Cercospora zaeae-maydis</i>	5860	Illinois	C. Naidoo
<i>Cercospora zaeae-maydis</i>	6939	Ohio	C. Naidoo
<i>Cercospora zaeae-maydis</i>	6911	Illinois	C. Naidoo
<i>Cercospora zaeae-maydis</i>	6928	Illinois	C. Naidoo
<i>Cercospora zaeae-maydis</i>	SKIN11	Indiana	L. Dunkle ⁶
<i>Cercospora zaeae-maydis</i>	Ladder 3-1	Indiana	L. Dunkle
<i>Cercospora zaeae-maydis</i>	POS12	Indiana	L. Dunkle

³American Type Culture Collection, Rockville, Maryland USA

⁴Syn. *Exserohilum turcicum*, *Bipolaris turcica*, *Drechslera turcica*

⁵Syn. *Drechslera zeicola*, *Bipolaris zeicola*

⁶Dr. Larry Dunkle, Purdue University, West Lafayette, Indiana USA

Table 1: (continued)

Source of Test Isolates			
Fungus	Isolate	Origin	Source
<i>Macrophomina phaseolina</i>	103	Kansas	J. Mihail ⁷
<i>Macrophomina phaseolina</i>	97	St. Charles, MO	J. Mihail
<i>Aspergillus flavus</i>	NRRL3557	--	G. Payne ⁸
<i>Fusarium moniliforme</i>	6354	Illinois	C. Naidoo
<i>Diplodia maydis</i>	5139	Iowa	C. Naidoo
<i>Puccinia sorghi</i>	IL	Illinois	C. Naidoo
<i>Puccinia sorghi</i>	MI	Michigan	C. Naidoo
<i>Puccinia sorghi</i>	IL88	Illinois	C. Naidoo
<i>Puccinia sorghi</i>	VA	Virginia	C. Naidoo
<i>Puccinia polyspora</i>	TX96	Texas	C. Naidoo

⁷ Dr. Jeanne Mihail, University of Missouri-Columbia, Columbia, Missouri USA⁸ Dr. Gary Payne, North Carolina State University, Raleigh, North Carolina USA**Example 2: Isolation of the Internal Transcribed Spacer (ITS) Regions**

The approximately 600 bp internal transcribed spacer region fragments were PCR amplified from 10 ng of genomic DNA isolated from *H. turcicum* isolates 6586, 26306 and 6402, *H. maydis* isolates 6921, 11534 and 24772, *H. carbonum* isolates 5870 and 16185, *K. zeae* isolates 56351, 18594 and 5125 and *C. zeae-maydis* isolates 5860, POS12 and Ladder 3-1 using 50 pmol of primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3'; SEQ ID NO:9) and ITS4 (5'-TCCTC-CGCTTATTGATATGC-3'; SEQ ID NO:12). PCRs were performed as described in Example 4. PCR products were purified using Promega's Wizard DNA Clean-up kit (Madison, WI). The DNA sequences of the ITS regions were determined by the dideoxy method using the Applied Biosystems (Foster City, CA) automated sequencer with the primers ITS1 (SEQ ID NO:9), ITS2 (5'-GCTGCGTTCTTCATCGATGC-3'; SEQ ID NO:10), ITS4 (SEQ ID NO:12) and the M13 universal -20 (5'-GTAAACGACGGCCAGT-3'; SEQ ID NO:13) and Reverse (5'-AACAGCTATGACCATG-3'; SEQ ID NO:14) primers. The ITS primers ITS1, ITS2, ITS3, and ITS4 used are detailed in White *et al.* (1990; In: PCR Protocols; Eds.: Innes *et al.* pages 315-322). PCR products from amplifications using *H. turcicum* isolate 26306, *H. maydis* isolates 11534 and 24772, *Kabatilla zeae* isolate 56351, *H. carbonum* isolate 16185, and *C. zeae-maydis* isolates POS12 and Ladder 3-1 were cloned using the Invitrogen Corporation's (San Diego, CA) TA Cloning Kit (part no. K2000-01) using the pCR11 or PCR2.1 cloning vector.

Example 3: DNA Extraction from Maize Leaves

DNA was extracted from maize leaves by using either a modified version of the Rapid DNA Extraction protocol from the MicroProbe Corporation's (Garden Grove, CA) IsoQuick Nucleic Acid Extraction Kit (cat# MXT-020-100) or by a bulk leaf maceration method. The Isoquick protocol was used to extract highly purified DNA from fungal inoculated maize leaves for assay validation purposes. Typical yields using the IsoQuick kit were 5-10 µg of total DNA from 0.2 g of leaf tissue from which a approximately 100 ng of total DNA were used in each PCR assay.

The bulk leaf maceration method was used to isolate DNA from several naturally infected maize leaves from the field to optimize the leaf field sampling method for high throughput analysis. In step 2 of this method, "Muller Extraction Buffer" is used. The potential concentration ranges of the ingredients of the Muller Extraction Buffer are as follows:

- 0-2.0 % w/v Tween-80
- 0-2.0 M Tris-Cl, pH 6-8
- 0-2.0 M NaCl
- 0-2 % BSA
- 0-2 % sodium azide
- 0-500 mM EDTA
- 0-2 % w/v tartrazin

However, in the preferred embodiment of the bulk leaf maceration method, the following recipe is used: 0.1% w/v

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Tween-80; 0.04 M Tris-Cl, pH 7.7; 0.15 M NaCl; 0.1% w/v BSA-Pentex fraction V; 0.01% w/v sodium azide; 200 mM EDTA. The color dye tartrazin may optionally be added as well.

Modified Rapid DNA Extraction:

Before using the kit for the first time, the entire contents of Reagent 2A (20 x Dye Concentrate) were added to Reagent 2 (Extraction Matrix).

- (1) Approximately 0.2 g of leaf sample were added to a 1.5 ml eppendorf tube containing 50 μ l sample buffer A and 50 μ l #1 lysis solution. The leaf sample was ground with a Kontes pestle.
- (2) Reagent 2 (Extraction Matrix) was shaken vigorously. 350 μ l of reagent 2 was added to the sample lysate.
- (3) 200 μ l of Reagent 3 were added (Extraction Buffer) to the sample. The sample was vortexed 20 sec.
- (4) Microcentrifugation at 12,000 x g for 5 min.
- (5) The aqueous phase (upper layer) was transferred to a new microcentrifuge tube. This volume was typically about 200 μ l.
- (6) 0.1 x the volume of the aqueous phase of Reagent 4 (Sodium Acetate) was transferred to the aqueous phase sample.
- (7) An equal volume of isopropanol was added to the aqueous phase sample followed by vortexing.
- (8) Microcentrifugation at 12,000 x g for 10 min.
- (9) The supernatant was discarded without disturbing the nucleic acid pellet. 0.5 ml of -20°C 70% ethanol was added to the pellet. The tube was vortexed to mix.
- (10) Microcentrifugation at 12,000 x g for 5 min.
- (11) The supernatant was discarded and the pellet was allowed to dry.
- (12) The nucleic acid pellet was dissolved in 50 μ l TE with 100 μ g/ml Rnase A.

Bulk Leaf Maceration Method:

- (1) Took a random sampling of an appropriate number of leaves from a population of maize plants.
- (2) Placed the leaves in a Bioreba (Reinach, Switzerland) heavy duty plastic bag (cat#490100). Weighed the plant tissue, plastic bag with leaves minus the tare (weight of the plastic bag).
- (3) Added an equal volume (ml) of Muller Extraction Buffer per weight (g) of leaf tissue. Macerated the tissue using a Bioreba Homex 6 homogenizer set at 70. Ground the leaves until the tissue was fibrous.
- (4) Removed maceration juice (extract) from the macerated tissue/extraction buffer.
- (5) Pooled the extracts from multiple bags, if used, and vortexed well. Aliquoted the extraction juice into eppendorf tubes on ice.
- (6) Boiled 100 μ l of the concentrated extract for 5 minutes.
- (7) Placed the boiled extract on ice.
- (8) Made a 1:10 dilution by adding 10 μ l from the boiled, concentrated extract to 90 μ l of sterile dH₂O.
- (9) Stored the diluted extracts on ice until ready to use.

Although the examples set forth herein describe using leaf tissue as the source of DNA, other plant tissue such as stem and root tissue could also be used in the above DNA extraction methods.

Example 4: Polymerase Chain Reaction Amplification

Polymerase chain reactions were performed with the GeneAmp Kit from Perkin-Elmer/Cetus (Norwalk, CT; part no. N808-0009) using 50 mM KCl, 2.5 mM MgCl₂, 10 mM Tris-HCl, pH8.3, containing 200 μ M of each dTTP, dATP, dCTP, and dGTP, 50 p mol each primer, 2.5 units of *Taq* polymerase and 10 ng of genomic DNA or 1 μ l of 1:10 diluted plant extract in a final volume of 50 μ l. Reactions were run for 30 - 40 cycles of 15 s at 94°C, 15 s at 50°C - 70°C, and 45 s at 72°C in a Perkin-Elmer/Cetus Model 9600 thermal cycler. The products were analyzed by loading 10 μ l of each PCR sample on a 1.0% agarose gel and electrophoresed.

Example 5: Synthesis and Purification of Oligonucleotides

Oligonucleotides (primers) were synthesized by either Integrated DNA Technologies (Coralville, IA) or Midland Certified Reagent Company (Midland, Texas).

Example 6: Selection of Species-Specific Primers

The ITS regions of *H. turcicum*, *H. maydis*, *H. carbonum* and *C. zeae-maydis* were aligned (Figure 1). Separate alignments were also made for each pathogen's isolates ' ITS regions (Figures 2-6). Oligonucleotide primers (Table 2) were synthesized according to Example 5 based on analysis of the aligned sequences. Primers were designed to the regions that contained the greatest differences in sequence among the fungal species. In addition, the published ribosomal gene-specific primers ITS1, ITS2, ITS3 and ITS4 (White *et al.*, 1990; In: PCR Protocols; Eds.: Innes *et al.* pages 315-322) were synthesized for testing in combination with the primers specific for the ITS region. Primers specific to the ITS regions of the published *Puccinia sorghi* sequence (Genbank accession#L08734, SEQ ID: 8) were also synthesized.

Table 2: Primer Design for Fungal Detection

	<u>Primer Template</u>	<u>Primer Name</u>	<u>Primer Sequence</u>
5	<i>H. turcicum</i>	JB588	5' TGGCAATCAGTGCTCTGCTG 3' (SEQ ID NO:15)
	<i>H. turcicum</i>	JB595	5' TCCGAGGTCAAAATGTGAGAG 3' (SEQ ID NO:24)
10	<i>H. maydis</i>	JB589	5' CCTTTTTTTTATGCAGTTGCA 3' (SEQ ID NO:18)
	<i>H. maydis</i>	JB591	5' CTCCTGATACAGAGTGCAAAA 3' (SEQ ID NO:20)
	<i>H. maydis</i>	JB596	5' GAGGTCAAAAGTTAAAAATCGTAA 3' (SEQ ID NO:25)
15	<i>Helmin. spp.</i>	JB588	5' CACCCATGTCTTTTGC GCAC 3' (SEQ ID NO:17)
	<i>Helmin. spp.</i>	JB587	5' CAGTTGCAATCAGCGTCAGTA 3' (SEQ ID NO:16)
	<i>H. carbonum</i>	JB592	5' CTCCTGATACAAAGCGCAAAT 3' (SEQ ID NO:21)
20	<i>H. carbonum</i>	JB590	5' CCTTTTTTTTATGCAGTTACC 3' (SEQ ID NO:19)
	<i>H. carbonum</i>	JB598	5' CCGAGGTCAAAAGTTAAAAATCTA 3' (SEQ ID NO:27)
	<i>H. carbonum</i>	JB597	5' GGCTCCAGTTTTCATTTTATAGAT 3' (SEQ ID NO:26)
25	<i>K. zeae</i>	JB616	5' TGTTGTTAAACTACCTTGTTGC 3' (SEQ ID NO:29)
	<i>K. zeae</i>	JB618	5' GTTCTGTGCGGCAGAAGTC 3' (SEQ ID NO:31)
	<i>K. zeae</i>	JB615	5' TTTGGCGGGACCGCTCGG 3' (SEQ ID NO:28)
	<i>K. zeae</i>	JB617	5' GAGTTAAACCAAACTCTTGTTG 3' (SEQ ID NO:30)
30	<i>K. zeae</i>	JB619	5' CGCCAGACGTTGATTGAATG 3' (SEQ ID NO:32)
	<i>C. zeae-maydis</i>	JB593	5' GGCCTTCGGGCTCGACCT 3' (SEQ ID NO:22)
	<i>C. zeae-maydis</i>	JB594	5' CGGACAGCTCAGCCGGAG 3' (SEQ ID NO:23)
35	<i>C. zeae-maydis</i>	JB620	5' CAACCCTTTGTGAACACAAC 3' (SEQ ID NO:33)
	<i>C. zeae-maydis</i>	JB621	5' CGCTCCGAAGCGATTAATG 3' (SEQ ID NO:34)
	<i>C. zeae-maydis</i>	JB622	5' TTCAAACACTGCATCTTTGCG 3' (SEQ ID NO:35)
40	<i>C. zeae-maydis</i>	JB623	5' AGATTTAGACGGCCGCGAC 3' (SEQ ID NO:36)
	<i>C. zeae-maydis</i>	JB626	5' GAGTGAGGGCCTTCGGGC 3' (SEQ ID NO:39)
	<i>C. zeae-maydis</i>	JB627	5' GCTTCGGGGGGCGACCC 3' (SEQ ID NO:40)
45	<i>C. zeae-maydis</i>	JB628	5' GACCGCCGCGCTCCG 3' (SEQ ID NO:41)
	<i>P. sorghi</i>	JB624	5' GTAGTCTCTATCTCAACAAC 3' (SEQ ID NO:37)
	<i>P. sorghi</i>	JB625	5' GTAAACAACCACCTTTAATTAT 3' (SEQ ID NO:38)
50	18S rDNA	ITS1	5' TCCGTAGGTGAACCTGCGG 3' (SEQ ID NO:9)
	5.8S rDNA	ITS2	5' GCTGCGTTCTTCATCGATGC 3' (SEQ ID NO:10)
55	5.8S rDNA	ITS3	5' GCATCGATGAAGAACGCAGC 3' (SEQ ID NO:11)

25S rDNA ITS4 5' TCCTCCGCTTATTGATATGC 3' (SEQ ID NO:12)

Note: *Helminthosporium* spp. includes *H. maydis*, *H. turcicum* and *H. carbonum*.

Example 7: Determination of Primer Specificity to Purified Fungal Genomic DNA

PCRs were performed according to Example 4 using different primer combinations (Table 3) in an attempt to amplify a single species-specific fragment. Species-specific PCR amplification products were produced from primers designed from the ITS region between the 18S and 25S ribosomal DNA subunits of each fungal strain of interest.

Table 3: ITS-Derived Diagnostic PCR Primers

Source of template DNA	5'Primer	3'Primer	Approximate size of amplified fragment
<i>H. turcicum</i>	JB586 (SEQ ID NO:15)	JB595 (SEQ ID NO:24)	485bp
<i>H. maydis</i>	JB589 (SEQ ID NO:18)	JB591 (SEQ ID NO:20)	348bp
<i>H. maydis</i>	JB589 (SEQ ID NO:18)	JB596 (SEQ ID NO:25)	397bp
<i>H. maydis</i>	JB588 (SEQ ID NO:17)	JB596 (SEQ ID NO:25)	463bp
<i>H. maydis</i>	JB588 (SEQ ID NO:17)	JB591 (SEQ ID NO:20)	413bp
<i>H. maydis</i>	JB587 (SEQ ID NO:16)	JB596 (SEQ ID NO:25)	331bp
<i>H. maydis</i>	JB587 (SEQ ID NO:16)	JB591 (SEQ ID NO:20)	333bp
<i>H. maydis</i>	JB588 (SEQ ID NO:17)	JB598 (SEQ ID NO:27)	465bp
<i>H. maydis</i>	JB587 (SEQ ID NO:16)	JB598 (SEQ ID NO:27)	375bp
<i>H. carbonum</i>	JB590 (SEQ ID NO:19)	JB598 (SEQ ID NO:27)	398bp
<i>H. carbonum</i>	JB590 (SEQ ID NO:19)	JB592 (SEQ ID NO:21)	346bp
<i>H. carb./H. maydis</i>	JB588 (SEQ ID NO:17)	JB598 (SEQ ID NO:27)	465bp
<i>H. carb./H. maydis</i>	JB587 (SEQ ID NO:16)	JB598 (SEQ ID NO:27)	384bp
<i>K. zeae</i>	JB616 (SEQ ID NO:29)	JB618 (SEQ ID NO:31)	455bp
<i>K. zeae</i>	JB615 (SEQ ID NO:28)	ITS4 (SEQ ID NO:12)	508bp
<i>K. zeae</i>	JB616 (SEQ ID NO:29)	ITS4 (SEQ ID NO:12)	531bp
<i>K. zeae</i>	JB617 (SEQ ID NO:30)	ITS4 (SEQ ID NO:12)	443bp
<i>K. zeae</i>	JB615 (SEQ ID NO:28)	JB618 (SEQ ID NO:31)	433bp
<i>K. zeae</i>	JB617 (SEQ ID NO:30)	JB618 (SEQ ID NO:31)	366bp
<i>K. zeae</i>	JB615 (SEQ ID NO:28)	JB619 (SEQ ID NO:32)	402bp

	<i>C. zeae-maydis</i>	JB593 (SEQ ID NO:22)	JB594 (SEQ ID NO:23)	380bp
5	<i>C. zeae-maydis</i>	JB620 (SEQ ID NO:33)	JB621 (SEQ ID NO:34)	393bp
	<i>C. zeae-maydis</i>	JB620 (SEQ ID NO:33)	JB623 (SEQ ID NO:36)	420bp
	<i>C. zeae-maydis</i>	JB622 (SEQ ID NO:35)	JB621 (SEQ ID NO:34)	320bp
10	<i>C. zeae-maydis</i>	JB593 (SEQ ID NO:22)	JB621 (SEQ ID NO:34)	415bp
	<i>C. zeae-maydis</i>	JB622 (SEQ ID NO:35)	JB594 (SEQ ID NO:23)	285bp
	<i>C. zeae-maydis</i>	JB593 (SEQ ID NO:22)	JB623 (SEQ ID NO:36)	442bp
15	<i>C. zeae-maydis</i>	JB626 (SEQ ID NO:39)	JB628 (SEQ ID NO:41)	427bp
	<i>C. zeae-maydis</i>	JB593 (SEQ ID NO:22)	ITS4 (SEQ ID NO:12)	558bp
	<i>P. sorghi</i>	JB624 (SEQ ID NO:37)	JB625 (SEQ ID NO:38)	409bp
20	<i>P. sorghi/Helm.spp.</i>	JB587 (SEQ ID NO:16)	ITS4 (SEQ ID NO:12)	434bp
	<i>P. sorghi/Helm.spp.</i>	JB588 (SEQ ID NO:17)	ITS4 (SEQ ID NO:12)	517bp

25 Note: *Helminthosporium* spp. includes *H. maydis*, *H. turcicum* and *H. carbonum*.

Example 8: Determination of Primer Specificity to Plant Tissue Infected with Fungi and Cross-Reactivity with Other Maize Fungal Pathogens

30 Total genomic DNA was isolated as described in Example 3 from healthy maize leaves and from maize leaves inoculated with either *H. turcicum*, *H. maydis*, *H. carbonum*, *K. zeae*, *C. zeae-maydis* or *P. sorghi*. PCRs were performed as described in Example 4 testing the primer combinations listed in Example 7 against DNA from the maize leaves. Purified fungal genomic DNAs were obtained as described in Example 1 and PCR assayed as described in Example 4 using the species-specific primers. Other fungal DNA species and isolates were tested for the species-specific primers ability to cross-react with them.

35 The *H. turcicum*-specific primers JB586 (SEQ ID NO:15) and JB595 (SEQ ID NO:24) amplified a 485 bp fragment from DNA from all of the isolates of *H. turcicum* listed in Table 1 and from *H. turcicum*-infected maize leaf tissue. The primer set did not amplify a diagnostic fragment from healthy maize leaf tissue nor from purified genomic DNA from *H. maydis*, *H. carbonum*, *K. zeae*, *C. zeae-maydis* and *P. sorghi*. The primers also did not amplify a diagnostic fragment from purified genomic DNA isolated from the common maize pathogens *F. moniliforme*, *M. phaseolina*, *A. flavus* nor *D. maydis*.

40 Similar diagnostic results were obtained with the *H. maydis*-specific primers JB589 (SEQ ID NO:18) and JB591 (SEQ ID NO:20). The primers amplified an approximately 346 bp fragment from *H. maydis*-infected maize tissue, as well as from purified genomic DNA isolated from all of the *H. maydis* isolates listed in Table 1. The primer combination JB589 and JB591 did not amplify any fragments from healthy maize tissue, nor from DNA from any of the following maize pathogens: *H. turcicum*, *H. carbonum*, *K. zeae*, *C. zeae-maydis*, *P. sorghi*, *F. moniliforme*, *M. phaseolina*, *A. flavus* and *D. maydis*.

45 The primer combination JB590 (SEQ ID NO:19) and JB598 (SEQ ID NO:27) amplified a 398 bp fragment from DNA from all of the *H. carbonum* isolates listed in Table 1 and from maize leaves infected with *H. carbonum*. The primer combination JB590 and JB598 did not amplify any fragments from healthy maize tissue, nor from DNA from any of the following maize pathogens: *H. turcicum*, *H. maydis*, *K. zeae*, *C. zeae-maydis*, *P. sorghi*, *F. moniliforme*, *M. phaseolina*, *A. flavus* and *D. maydis*.

50 The *K. zeae*-specific primers JB616 (SEQ ID NO:29) and JB618 (SEQ ID NO:31) amplified a 455 bp fragment from DNA from all of the isolates of *K. zeae* isolates listed in Table 1 and from *K. zeae*-infected maize leaf tissue. The primer set did not amplify a diagnostic fragment from healthy maize leaf tissue nor from purified genomic DNA from *H. maydis*, *H. carbonum*, *H. turcicum*, *C. zeae-maydis* and *P. sorghi*. The primers also did not amplify a diagnostic fragment from purified genomic DNA isolated from the common maize pathogens *F. moniliforme*, *M. phaseolina*, *A. flavus* nor *D. maydis*.

The primer combination JB593 (SEQ ID NO:22) and JB621 (SEQ ID NO:34) amplified a 415 bp fragment from DNA from all of the *C. zeae-maydis* isolates listed in Table 1 and from maize leaves infected with *C. zeae-maydis*. The primer combination JB593 and JB621 did not amplify any fragments from healthy maize tissue, nor from DNA from any of the following maize pathogens: *H. turcicum*, *H. maydis*, *K. zeae*, *H. carbonum*, *P. sorghi*, *F. moniliforme*, *M. phaseolina*, *A. flavus* and *D. maydis*.

The primer combination JB624 (SEQ ID NO:37) and JB625 (SEQ ID NO:38) amplified a 409 bp fragment from all of the *P. sorghi* isolates listed in Table 1 and from *P. sorghi*-infected maize leaf tissue. The primers did not amplify from *P. polyspora*, *H. turcicum*, *H. maydis*, *K. zeae*, *H. carbonum*, *F. moniliforme*, *M. phaseolina*, *A. flavus* and *D. maydis*. The primers also did not amplify from healthy maize tissue.

Primers JB587 (SEQ ID NO:16) and ITS4 (SEQ ID NO:12) amplified a 434 bp fragment from *P. sorghi*, *H. turcicum*, *H. maydis* and *H. carbonum* but not from the other following maize pathogens: *K. zeae*, *F. moniliforme*, *M. phaseolina*, *A. flavus* and *D. maydis*. The primers also amplified a 434 bp fragment from maize infected with *P. sorghi*, *H. turcicum*, *H. maydis* and *H. carbonum* but did not amplify any fragments from healthy maize tissue. While the present invention has been described with reference to specific embodiments thereof, it will be appreciated that numerous variations, modifications, and further embodiments are possible, and accordingly, all such variations, modifications and embodiments are to be regarded as being within the scope of the present invention.

DEPOSITS

The following deposits were made on November 06, 1996, at Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, U.S.A.:

1. *E. coli* DH5α (pCRCZLAD3-1(4-3); SEQ ID NO:1): Accession No. NRRL B-21645
2. *E. coli* DH5α (pCRCZMPOS12(2-1); SEQ ID NO:2): Accession No. NRRL B-21641
3. *E. coli* DH5α (pCRKZ56351(5-1); SEQ ID NO:3): Accession No. NRRL B-21646
4. *E. coli* DH5α (pCRHMAY24772(2-1); SEQ ID NO:4): Accession No. NRRL B-21642
5. *E. coli* DH5α (pCRHMAy11534(4-1); SEQ ID NO:5): Accession No. NRRL B-21644
6. *E. coli* DH5α (pCRHTUR26306(3-1); SEQ ID NO:6): Accession No. NRRL B-21643
7. *E. coli* DH5α (pCRHCAR16185(5-2); SEQ ID NO:7): Accession No. NRRL B-21647

Annex to the description

SEQUENCE LISTING

((1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NOVARTIS AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4058
- (G) TELEPHONE: +4161 324 11 11
- (H) TELEFAX: + 4161 322 75 32

(ii) TITLE OF INVENTION: Detection of Maize Fungal Pathogens
Using the Polymerase Chain Reaction

(iii) NUMBER OF SEQUENCES: 41

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

((2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: Cercospora zeae-maydis
- (C) INDIVIDUAL ISOLATE: Ladder 3-1

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pCRCZLAD3-1(4-3)

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(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 1..30

(D) OTHER INFORMATION: /note= "3' end of small subunit
rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 31..175

(D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 176..332

(D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 333..478

(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 479..535

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCCCGGAGGC CTTCAAACAC GCATCTTTGC GTCGGAGTTT AAGTAAATTA AACAAAACCTT	180
TCAACAACGG ATCTCTTGGT TCTGGCATCG ATGAAGAAGC CAGCGAAATG CGATAAGTAA	240
TGTGAATTGC AGAATTCAGT GAATCATCGA ATCTTTGAAC GCATATTGCG CCCTTTGGTA	300
TTCCGAAGGG CATGCCTGTT CGAGCGTCAT TTCACCACTC AAGCCTAGCT TGGTACTGGG	360
CGCCGCGGTG TTCCGCGCGC CTTAAAGTCT CCGGCTGAGC TGTCCGTCTC TAAGCGTTGT	420

GATTTTCATTA ATCGCTTCGG AGCGCGGGCG GTCGCGGCCG TTAAATCTTT CACAAGGTTG 480

ACCTCGGATC AGGTAGGGAT ACCCGCTGAA CTTAAGCATA TCAATAAGCG GAGGA 535

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: *Cercospora zeae-maydis*
- (C) INDIVIDUAL ISOLATE: POS 12

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pCRCZMPOS12(2-1)

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "3' end of small subunit

rRNA gene"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 31..176
- (D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 177..333
- (D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 334..479
- (D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 480..536

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCGTAGGTG AACCTGCGGA GGGATCATT CTGAGTGAGG GCCTTCGGGC TCGACCTCCA	60
ACCCCTTTGTG AACACAACCT GTTGCTTCGG GGGCGACCCT GCCGTTCCGA CGGCGAGCGC	120
CCCCGGAGGC CTTCAAACAC TGCATCTTTG CGTCGGAGTT TAAGTAAATT AAACAAACT	180
TTCAACAACG GATCTCTTGG TTCTGGCATC GATGAAGAAC GCAGCGAAAT GCGATAAGTA	240
ATGTGAATTG CAGAATTCAG TGAATCATCG AATCTTTGAA CGCATATTGC GCCCTTTGGT	300
ATTCCGAAGG GCATGCCTGT TCGAGCGTCA TTTCACCACT CAAGCCTAGC TTGGTATTGG	360
GCGCCGCGGT GTTCCGCGCG CCTTAAAGTC TCCGGCTGAG CTGTCCGTCT CTAAGCGTTG	420
TGATTTCAAT AATCGCTTCG GAGCGCGGGC GGTGCGGGCC GTTAAATCTT TCACAAGGTT	480
GACCTCGGAT CAGGTAGGGA TACCCGCTGT ACTTAAGCAT ATCAATAAGC GGAGGA	536

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: Kabatiella zeae

(C) INDIVIDUAL ISOLATE: 56351

(vii) IMMEDIATE SOURCE:

(B) CLONE: pCRKZ56351(5-1)

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(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 1..30

(D) OTHER INFORMATION: /note= "3' end of small subunit
rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 31..217

(D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 218..373

(D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 374..540

(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 541..597

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40	TCCGTAGGTG AACCTGCGGA AGGATCATTA AAGAGTAAGG GTGCCAGCG CCCGACCTCC	60
	AACCCTTTGT TGTAAACT ACCTTGTTC TTTGGCGGA CCGCTCGGTC CCCGAGCCGC	120
45	CGGGGGGATC CGTCCCCCAT GCGAGCGCC CGCCGGAGTT AAACCAACT CTTGTTGAAC	180
	AAACCGGTCG TCTGAGTTAA AATTTTGAAT AAATCAAAC TTTCAACAAC GGATCTCTTG	240
50	GTTCTCGCAT CGATGAAGAA CGCAGCGAAA TGCATAAGT AATGTGAATT GCAGAATTCA	300
	GTGAATCATC GAATCTTTGA ACGCACATTG CGCCCTTGG TATTCGAGG GGCATGCCTG	360

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TTCGAGCGTC ATTACACCAC TCAAGCTCTG CTTGGTATTG GCGTCCGTC CTTTCGGGGG 420
 5 CGCGCCTCAA ACACCTCGGC GAGGCCTCAC CGGCTTCAGG CGTAGTAGAA TTCATTCAAT 480
 CAACGTCTGG CGAAACCGGA GGGGACTTCT GCCGACAGAA ACCTTTTATA TTTTCTAGGT 540
 10 TGACCTCGGA TCAGGTAGGG ATACCCGCTG AACTTAAGCA TATCAATAAG CGGAGGA 597

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: Helminthosporium maydis
- (C) INDIVIDUAL ISOLATE: 24772

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pCRHMAY24772(2-1)

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "3' end of small subunit rRNA gene"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 31..200
- (D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

- (A) NAME/KEY: misc_RNA
- (B) LOCATION: 201..358
- (D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION: 359..531

(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 532..588

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGTAGGTG AACCTGCCGA GGGATCATT A CACAACAAA TATGAAGGCC TGGCTTTGCG	60
GCCGGCTGAA ATATTTT TTTT CACCCATGTC TTTTGCACAC TTGTTGTTTC CTGGGCGGGT	120
TCGCCCCGCA CCAGGACCAA ACCCTAAACC TTTT TTTTAT GCAGTTGCAW TCAGCGTCAG	180
TATAACAAT GTAATTATTA CAAC TTCAA CAACGGATCT CTTGGTTCTG GCATCGATGA	240
AGAACGCAGC GAAATGCGAT ACGTAGTGTG AATTGCAGAA TTCAGTGAAT CATCGAATCT	300
TTGAACGCAC ATTGCGCCCT TTGGTAT TCC AAAGGGCATG CCTGTTGAG CGTCATTGT	360
ACCCTCAAGC TTTGCTTGGT GTTGGGCGTT TTTGTCTCCC TCTTTGCTGG GAGACTCGCC	420
TTAAAACGAW TGGCAGCCGG CCTACTGGTT TCGGAGCGCA GCACATATTT TGCACTCTGT	480
ATCAGGAGAA AAGGACGGTA ATCCATCAAG ACTCTTACGA TTTT TAACTT TTGACCTCGG	540
ATCAGGTAGG GAYACCCGCT GAACTTAAGC ATATCAATAA GCGGAGGA	588

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

EP 0 859 061 A2

(B) STRAIN: Helminthosporium maydis

(C) INDIVIDUAL ISOLATE: 11534

(vii) IMMEDIATE SOURCE:

(B) CLONE: pCRHMAY11534(4-1)

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 1..30

(D) OTHER INFORMATION: /note= "3' end of small subunit
rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 31..200

(D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 201..358

(D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 359..531

(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 532..588

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCGTAGGTG AACCTGCGGA GGGATCATTA CACAACAAA TATGAAGGCC TGGCTTTGCG	60
GCCGGCTGAA ATATTTTTTT CACCCATGTC TTTTGCGCAC TTGTTGTTTC CTGGGCGGGT	120
TCGCCCGCCA CCAGGACCAA ACCATAAACC TTTTTTTTAT GCAGTTGCAA TCAGCGTCAG	180
TATAACAAT GTAATTATTA CAACTTTCAA CAACGGATCT CTTGGTTCTG GCATCGATGA	240

AGAACGCAGC GAAATGCGAT ACGTAGTGTG AATTGCAGAA TTCAGTGAAT CATCGAATCT 300
5 TTGAACGCAC ATTGCGCCCT TTGGTATTCC AAAGGGCATG CCTGTTCGAG CGTCATTTGT 360
ACCCTCAAGC TTTGCTTGGT GTTGGGCGTT TTTGTCTCCC TCTTTGCTGG GAGACTCGCC 420
10 TTAAAACGAT TGGCAGCCGG CCTACTGGTT TCGGAGCGCA GCACATATTT TGCACTCTGT 480
ATCAGGAGAA AAGGACGGTA ATCCATCAAG ACTCTTACGA TTTTAACTT TTGACCTCGG 540
15 ATCAGGTAGG GATACCCGCT GAACTTAAGC ATATCAATAA GCGGAGGA 588

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
30 (vi) ORIGINAL SOURCE:
(B) STRAIN: Helminthosporium turcicum
(C) INDIVIDUAL ISOLATE: 26306
35 (vii) IMMEDIATE SOURCE:
(B) CLONE: pCRHTUR26306(3-1)
(ix) FEATURE:
40 (A) NAME/KEY: misc_RNA
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "3' end of small subunit
rRNA gene"
45 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 31..199
50 (D) OTHER INFORMATION: /note= "ITS 1"
(ix) FEATURE:
(A) NAME/KEY: misc_RNA
55

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(B) LOCATION: 200..356
(D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 357..523
(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA
(B) LOCATION: 524..580
(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGTAGGTG AACCTGCGGA GGGATCATTA CACAAAGATA TGAAGGTAGG GTACTGGCAA	60
CAGTGCTCTG CTGAAATATT TTCACCCATG TCTTTTGCGC ACTTTTGTGTT TCCTGGGCGA	120
GTTTGCTCGC CACCAGGACC CCCATATGAA CCTTTTTTGT TTTTGCACTC AGCGTCAGTA	180
CAATAATTTA ATCTATTAAA ACTTTCAACA ACGGATCTCT TGGTCTGGC ATCGATGAAG	240
AACGCAGCGA AATGCGATAC GTAGTGTGAA TTGCAGAATT CAGTGAATCA TCGAATCTTT	300
GAACGCACAT TCGGCCCTTT GGTATTCCAA AGGGCATGCC TGTTCGAGCG TCATTTGTAC	360
CCTCAAGCTT TGCTTGGTGT TGGGCGTCTT ATTGTCTCTC CGTCTCGGGG AGACTCGCCT	420
TAAACAATT GGCAGCCGGC CTACTGGTTT CGGAGCGCAG CACAAATTTG CGCTTGCAAT	480
CAGCCAAGGG CGGCATCCAT GAAGCCTTTT TTCTCTCACA TTTTGACCTC GGATCAGGTA	540
GGGATACCCG CTGAACTTAA GCATATCAAT AAGCGGAGGA	580

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: Helminthosporium carbonum

(C) INDIVIDUAL ISOLATE: 16185

(vii) IMMEDIATE SOURCE:

(B) CLONE: pCRHCAR16185(5-2)

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 1..30

(D) OTHER INFORMATION: /note= "3' end of small subunit
rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 31..202

(D) OTHER INFORMATION: /note= "ITS 1"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 203..360

(D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 361..530

(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA

(B) LOCATION: 531..587

(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCGTAGGTG AACCTGCGGA GGGATCATTA CACAACAAA TATGAAGGCC CTGGCTTCGC

60

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GGCCGGCTGA AATATTTTTT CACCCATGTC TTTTGCAC TGTGTGTTT CTGGGCGGGT 120
 5 TTGCCCAGCA CCAGGACCAA ACCATAAACC TTTTTTTT TGCAGTTACC ATCAGCGTCA 180
 GTAAAAACAA TGTAAATTAAT TACAACCTTC AACACGGAT CTCTTGGTTC TGGCATCGAT 240
 10 GAAGAACGCA GCGAAATGCG ATACGTAGTG TGAATTGCAG AATTCAGTGA ATCATCGAAT 300
 CTTTGAACGC ACATTGCGCC CTTTGGTATT CCAAAGGGCA TGCCTGTTCTG AGCGTCATTT 360
 15 GTACCTTCAA GCTTTGCTTG GTGTGGGCG TTTTGTCTC CCTCTTCTG GGAGACTCGC 420
 CTTAAACGA TTGGCAGCCG GCCTACTGGT TTCGGAGCGC AGCACATAAT TTGCGCTTTG 480
 20 TATCAGGAGA AAAGGACGGT AATCCATCAA GACTCTAGAT TTTTAACTTT TGACCTCGGA 540
 TCAGGTAGGG ATACCCGCTG AACTTAAGCA TATCAATAAG CGGAGGA 587

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: Puccinia sorghi
- (C) INDIVIDUAL ISOLATE: SZZI11

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /note= "partial ITS 1"

(ix) FEATURE:

- (A) NAME/KEY: misc_rna
- (B) LOCATION: 46..201
- (D) OTHER INFORMATION: /note= "5.8S rRNA gene"

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
(B) LOCATION: 202..441
(D) OTHER INFORMATION: /note= "ITS 2"

(ix) FEATURE:

(A) NAME/KEY: misc_RNA
(B) LOCATION: 442..458
(D) OTHER INFORMATION: /note= "5' end of large subunit
rRNA gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACACAAGTTT AAAAGAATGT AAACAACCAC CTTTAATTAT AAAAATAACT TTTAACAATG 60
GATCTCTAGG CTCTCACATC GATGAAGAAC ACAGTGAAAT GTGATAAGTA ATGTGAATTG 120
CAGAATTCAG TGAATCATCG AATCTTTGAA CGCATCTTGC GCCTTTTGGT ATTCCAAAAG 180
GCACACCTGT TTGAGTGTCA TGAAACCCTC TCACAAAATA AATAATTTTT ATTATGATTT 240
TTGTGGATGT TGAGTGCTGC TGTGTTACAC ATAGCTCACT TTAAATGTAT AAGTCATCTT 300
CTTTATATAG CAAAAAGAA GAGATGGATT GACTTGATGT GTAATAATTT TTTTTCATCA 360
CATTGAGGAA AGTAGCAATA CTTGCCATCT TTATATTATT TTGTTGTTGA GATAGAGACT 420
ACTAAACAAA CAATTTAAAA TTTAAGACCT CAAATCAG 458

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer ITS1"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCCGTAGGTG AACCTGCGG

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer ITS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGCGTTCT TCATCGATGC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer ITS3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCATCGATGA AGAACGCAGC

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer ITS4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCTCCGCTT ATTGATATGC

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "M13 universal-20 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAAAACGAC GGCCAGT

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Reverse primer used in

Example 2"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10

AACAGCTATG ACCATG

16

(2) INFORMATION FOR SEQ ID NO:15:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(A) DESCRIPTION: /desc = "primer JB586"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGCAATCAG TGCTCTGCTG

20

35

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB587"

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

55

CAGTTGCAAT CAGCGTCAGT A

21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB588"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACCCATGTC TTTTGCAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB589"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTTTTTTTT ATGCAGTTGC A

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB590"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15

CCTTTTTTTT TATGCAGTTA CC

22

(2) INFORMATION FOR SEQ ID NO:20:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

30

(A) DESCRIPTION: /desc = "primer JB591"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTCCTGATAC AGAGTGCAAA A

21

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB592"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

5 CTCCTGATAC AAAGCGCAAA T 21

(2) INFORMATION FOR SEQ ID NO:22:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer JB593"
 20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCCTTCGGG CTCGACCT 18

30 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer JB594"

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

50 CGGACAGCTC AGCCGGAG 18

(2) INFORMATION FOR SEQ ID NO:24:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB595"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCCGAGGTCA AAATGTGAGA G

21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB596"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGTCAAAA GTTAAAAATC GTAA

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB597"

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTCCAGTT TTCAATTTTT AGAT

24

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB598"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCGAGGTCAA AAGTTAAAAA TCTA

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB615"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTTGGCGGGA CCGCTCGG

18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB616"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGTTGTTAAA ACTACCTTGT TGC

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB617"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGTTAAACC AAACCTTTGT TG

22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB618"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15

GTTTCTGTCTG GCAGAAGTC

19

(2) INFORMATION FOR SEQ ID NO:32:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB619"

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGACGT TGATTGAATG

40

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

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(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer JB620"

55

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:33:

5 CAACCCTTTG TGAACACAAC 20

(2) INFORMATION FOR SEQ ID NO:34:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: other nucleic acid
20 (A) DESCRIPTION: /desc = "primer JB621"

25 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGCTCCGAAG CGATTAATG 19

30 (2) INFORMATION FOR SEQ ID NO:35:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer JB622"

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 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

50 TTCAAACACT GCATCTTTGC G 21

55

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB623"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AGATTTAGAC GGCCGCGAC

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer JB624"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTAGTCTCTA TCTCAACAAC

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB625"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTAAACAACC ACCTTTAATT AT

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB626"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAGTGAGGGC CTTCGGGC

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB627"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 GCTTCGGGGG GCGACCC

17

(2) INFORMATION FOR SEQ ID NO:41:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer JB628"

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GACCGCCCGC GCTCCG

16

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Claims

- 35 1. An Internal Transcribed Spacer sequence selected from the group consisting of ITS1 and ITS2 of *Helminthosporium carbonum*; ITS1 and ITS2 of *Helminthosporium turoicum*; ITS1 and ITS2 of *Helminthosporium maydis*; ITS1 and ITS2 of *Cercospora zeae-maydis*; and ITS1 and ITS2 of *Kabatella zeae*.
- 40 2. An Internal Transcribed Spacer sequence selected from the group consisting of ITS1 of SEQ ID NO:1; ITS2 of SEQ ID NO:1; ITS1 of SEQ ID NO:2; ITS2 of SEQ ID NO:2; ITS1 of SEQ ID NO:3; ITS2 of SEQ ID NO:3; ITS1 of SEQ ID NO:4; ITS2 of SEQ ID NO:4; ITS1 of SEQ ID NO:5; ITS2 of SEQ ID NO:5; ITS1 of SEQ ID NO:6; ITS2 of SEQ ID NO:6; ITS1 of SEQ ID NO:7; and ITS2 of SEQ ID NO:7.
- 45 3. An oligonucleotide primer for use in amplification-based detection of a fungal Internal Transcribed Spacer DNA sequence, wherein said primer has sequence identity with at least about 5-10 nucleotides of the sequence of claim 2.
4. An oligonucleotide primer selected from the group consisting of SEQ ID NOs: 15 to 41.
- 50 5. A pair of oligonucleotide primers for use in the amplification-based detection of a fungal Internal Transcribed Spacer DNA sequence, wherein at least one of said primers is the oligonucleotide primer of claim 4.
6. The pair of oligonucleotide primers according to claim 5, wherein said pair is selected from the primer pairs listed in Table 3.
- 55 7. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *H. turoicum*, and wherein said pair comprises SEQ ID NO:15 and SEQ ID NO:24.
8. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *H. maydis*,

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and wherein one primer is selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:18 and the other primer is selected from the group consisting of SEQ ID NO:20, SEQ ID NO:25, and SEQ ID NO:27.

- 5 9. The pair of oligonucleotide primers according to claim 8, wherein said pair comprises SEQ ID NO:18 and SEQ ID NO:20.
- 10 10. The pair of oligonucleotide primers according to claim 8, wherein said pair of primers are used to detect *H. carbonum*, and wherein one primer is selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:19 and the other primer is selected from the group consisting of SEQ ID NO:21 and SEQ ID NO:27.
- 11 11. The pair of oligonucleotide primers according to claim 10, wherein said pair comprises SEQ ID NO:19 and SEQ ID NO:27.
- 15 12. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *K. zeae*, and wherein one primer is selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, and SEQ ID NO:30 and the other primer is selected from the group consisting of SEQ ID NO:12, SEQ ID NO:31, and SEQ ID NO:32.
- 20 13. The pair of oligonucleotide primers according to claim 12, wherein said pair comprises SEQ ID NO:29 and SEQ ID NO:31.
- 25 14. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *K. zeae-maydis*, and wherein one primer is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:33, SEQ ID NO:35, and SEQ ID NO:39 and the other primer is selected from the group consisting of SEQ ID NO:12, SEQ ID NO:23, SEQ ID NO:34, SEQ ID NO:36, and SEQ ID NO:41.
- 30 15. The pair of oligonucleotide primers according to claim 14, wherein said pair comprises SEQ ID NO:22 and SEQ ID NO:34.
16. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *P. sorghi*, and wherein said pair comprises SEQ ID NO:37 and SEQ ID NO:38.
- 35 17. The pair of oligonucleotide primers according to claim 6, wherein said pair of primers are used to detect *P. sorghi* and *Helminthosporium spp.*, and wherein said pair comprises SEQ ID NO:16 and SEQ ID NO:12.
18. A method for the detection of a fungal pathogen, comprising the steps of:
- (a) isolating DNA from a plant leaf infected with a pathogen;
- (b) subjecting said DNA to polymerase chain reaction amplification using at least one primer according to claims 3 or 4; and
- 40 (c) detecting said fungal pathogen by visualizing the product or products of said polymerase chain reaction amplification.
19. The method of claim 18, wherein said fungal pathogen is selected from the group consisting of: *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zeae-maydis*, *Kabatiella zeae*, and *Puccinia sorghi*.
- 45 20. A method for the detection of a fungal pathogen, comprising the steps of:
- (a) isolating DNA from a plant leaf infected with a pathogen;
- 50 (b) amplifying a part of the Internal Transcribed Spacer sequence of said pathogen using said DNA as a template in a polymerase chain reaction with a pair of primers according to any one of claims 5-17; and
- (c) detecting said fungal pathogen by visualizing the amplified part of the Internal Transcribed Spacer sequence.
- 55 21. The method of claim 20, wherein said fungal pathogen is selected from the group consisting of: *Helminthosporium carbonum*, *Helminthosporium turcicum*, *Helminthosporium maydis*, *Cercospora zeae-maydis*, *Kabatiella zeae*, and *Puccinia sorghi*.

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22. A diagnostic kit used in detecting a fungal pathogen, comprising the primer of any one of claims 3-5.
23. A diagnostic kit used in detecting a fungal pathogen, comprising a pair of oligonucleotide primers of any one of claims 5-17.
24. An extraction buffer solution for use in isolating DNA from an organism, comprising:
- (a) 0-2 % w/v Tween-80;
 - (b) 0-2 M Tris-Cl, pH 6-8;
 - (c) 0-2 M NaCl;
 - (d) 0-2 % BSA;
 - (e) 0-2 % sodium azide; and
 - (f) 0-500 mM EDTA.
25. The extraction buffer of claim 24, comprising: 0.1% w/v Tween-80; 0.04 M Tris-Cl, pH 7.7; 0.15 M NaCl; 0.1% w/v BSA-Pentex fraction V; 0.01% w/v sodium azide; and 200 mM EDTA.
26. The extraction buffer of claim 24, further comprising 0-2 % w/v tartrazin.
27. A method for extracting DNA from tissue, comprising the steps of:
- (a) taking a plurality of random tissue samples from an organism population;
 - (b) adding the extraction buffer of claim 25 to the tissue samples;
 - (c) macerating the tissue samples and extraction buffer to form an extract;
 - (d) removing the extract from the macerated tissue and buffer;
 - (e) boiling the extract; and
 - (f) diluting the extract to a concentration optimal for PCR analysis.
28. The method of claim 27, wherein the organism population is a plant population.
29. The method of claim 28, wherein the tissue samples are selected from leaves, stems, and roots.
30. The method of claim 28, wherein the extraction buffer comprises 0.1% w/v Tween-80; 0.04 M Tris-Cl, pH 7.7; 0.15 M NaCl; 0.1% w/v BSA-Pentex fraction V; 0.01% w/v sodium azide; and 200 mM EDTA.

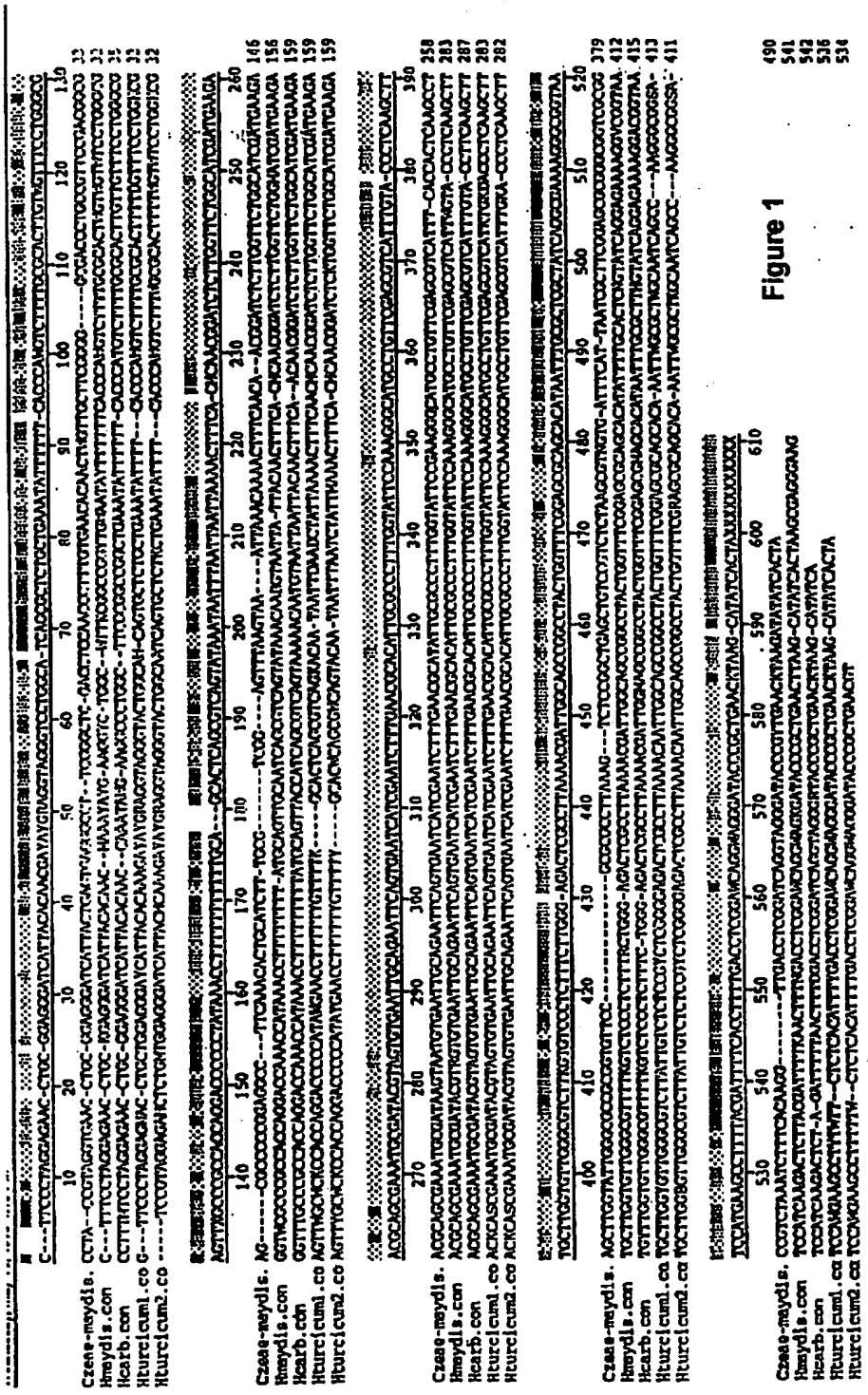


Figure 1

555

[illegible]

Figure 4

528
536
535

CZ45860. CON
 CZ45860-1 (2-1)
 CZ45860-2 (2-1)
 CZ45860-3 (2-1)
 CZ45860-4 (2-1)
 CZ45860-5 (2-1)
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Figure 5

160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
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10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	
10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160																									

Figure 6